



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Boyle, William J.
- (ii) TITLE OF INVENTION: Osteoprotegerin Binding Proteins
- (iii) NUMBER OF SEQUENCES: 39
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Amgen Inc.
 - (B) STREET: One Amgen Center Drive
 - (C) CITY: Thousand Oaks
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 91320-1789
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Winter, Robert B.
 - (C) REFERENCE/DOCKET NUMBER: A-451G

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asp Pro Asn Arg Gln Asp Ile Asp
1 5

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

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MATRIX CUSTOMER
SERVICE CENTER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTTCTCCTCA TATGGATCCA AACCGTATTT CTGAAGACAG CACTCACTGC TT

52

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TACGCACTCC GCGGTTAGTC TATGTCCTGA ACTTTGA

37

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Asn Ala Gly Gln Asp Ile Asp
1 5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATTTGATTCT AGAAGGAGGA ATAACATATG CATGAAAACG CAGGTCTGCA G

51

B1
Cont.

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TATCCGCGGA TCCTCGAGTT AGTCTATGTC CTGAACTTTG AA

42

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Glu Asp Thr Leu Gln Asp Ile Asp
1 5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATTTGATTCT AGAAGGAGGA ATAACATATG TCTGAAGACA CTCTGCCGGA CTCC

54

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

B1
Cont.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys Gln Ala Phe Gln Gln Asp Ile Asp
1 5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATTGATTCT AGAAGGAGGA ATAACATATG AAACAAGCTT TTCAGGGG

48

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Lys Glu Leu Gln His Gln Asp Ile Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATTGATTCT AGAAGGAGGA ATAACATATG AAAGAACTGC AGCACATTGT G

51

31
Cont.

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Gln	Arg	Phe	Ser	Gly	Gln	Asp	Ile	Asp
1				5					10

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATTTGATTCT AGAAGGAGGA ATAACATATG CAGCGTTTCT CTGGTGCTCC A

51

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Glu	Gly	Ser	Trp	Gln	Asp	Ile	Asp
1				5				

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

B1
Cont.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTTCTCCTCA TATGGAAGGT TCTTGTTGG ATGTGGCCCA

40

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Arg Gly Lys Pro Gln Asp Ile Asp
1 5

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTTCTCCTCA TATGCGTGGT AAACCTGAAG CTCAACCATT TGCA

44

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Lys Pro Glu Ala Gln Asp Ile Asp
1 5

B1
Cont.

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GTTCTCCTCA TATGAAACCT GAAGCTCAAC CATTTGCACA CCTCACCATC AAT

53

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met His Leu Thr Ile Gln Asp Ile Asp
1 5

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTTCTCCTCA TATGCATTTA ACTATTAACG CTGCATCTAT CCCATCGGGT TCCCATAAAG

60

TCACT

65

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

B1
cont.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Thr Ile Asn Ala Gln Asp Ile Asp
1 5

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTTCTCCTCA TATGACTATT AACGCTGCAT CTATCCCATC GGGTTCCCAT AAAGTCACT

59

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Lys Pro Glu Ala Gln Pro Phe Ala His
1 5 10

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCTCTAGGCC TGTACTTTTCG AGCGCAGATG

30

B!
cont.

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCTCTGCGGC CGCGTCTATG TCCTGAACTT TG

32

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCTCTCTCGA GTGGACAACC CAGAAGCCTG AGGCCAGCC ATTGTC

46

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCTCTGCGGC CGCGTCTATG TCCTGAACTT TG

32

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

B1
cont.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGCTTCCACC ATGAACAAGT GGCTGTGCTG CGCACTCCTG GTGCTCCTGG ACATCA

56

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TCGATGATGT CCAGGAGCAC CAGGAGTGC GAGCACAGCC ACTTGTCAT GGTGGA

56

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu Ser Ser
1 5 10 15

Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser
20 25

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu Ser Ser
1 5 10 15

Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Cys
20 25

31
cont.

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu
 1 5 10 15
 Met

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu
 1 5 10 15
 Met Cys

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2295 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 158..1105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAGCTCGGAT CCACTACTCG ACCACGCGT CCGGCCAGGA CCTCTGTGAA CCGGTCGGGG 60
 CGGGGGCCGC CTGGCCGGGA GTCTGCTCGG CGGTGGGTGG CCGAGGAAGG GAGAGAACGA 120

B1
Cont.

TCGCGGAGCA GGGCGCCCGA ACTCCGGGGCG CCGCGCC																ATG Met	CGC Arg	CGG Arg	GCC Ala	AGC Ser	CGA Arg	175
																1				5		
GAC Asp	TAC Tyr	GGC Gly	AAG Lys	TAC Tyr	CTG Leu	CGC Arg	AGC Ser	TCG Ser	GAG Glu	GAG Glu	ATG Met	GGC Gly	AGC Ser	GGC Gly	CCC Pro	223						
																10			20			
GGC Gly	GTC Val	CCA Pro	CAC His	GAG Glu	GGT Gly	CCG Pro	CTG Leu	CAC His	CCC Pro	GCG Ala	CCT Pro	TCT Ser	GCA Ala	CCG Pro	GCT Ala	271						
																25			30			
CCG Pro	GCG Ala	CCG Pro	CCA Pro	CCC Pro	GCC Ala	GCC Ala	TCC Ser	CGC Arg	TCC Ser	ATG Met	TTC Phe	CTG Leu	GCC Ala	CTC Leu	CTG Leu	319						
																40			45			
GGG Gly	CTG Leu	GGA Gly	CTG Leu	GGC Gly	CAG Gln	GTG Val	GTC Val	TGC Cys	AGC Ser	ATC Ile	GCT Ala	CTG Leu	TTC Phe	CTG Leu	TAC Tyr	367						
																55			60		70	
TTT Phe	CGA Arg	GCG Ala	CAG Gln	ATG Met	GAT Asp	CCT Pro	AAC Asn	AGA Arg	ATA Ile	TCA Ser	GAA Glu	GAC Asp	AGC Ser	ACT Thr	CAC His	415						
																75			80		85	
TGC Cys	TTT Phe	TAT Tyr	AGA Arg	ATC Ile	CTG Leu	AGA Arg	CTC Leu	CAT His	GAA Glu	AAC Asn	GCA Ala	GGT Gly	TTG Leu	CAG Gln	GAC Asp	463						
																90			95		100	
TCG Ser	ACT Thr	CTG Leu	GAG Glu	AGT Ser	GAA Glu	GAC Asp	ACA Thr	CTA Leu	CCT Pro	GAC Asp	TCC Ser	TGC Cys	AGG Arg	AGG Arg	ATG Met	511						
																105			110		115	
AAA Lys	CAA Gln	GCC Ala	TTT Phe	CAG Gln	GGG Gly	GCC Ala	GTG Val	CAG Gln	AAG Lys	GAA Glu	CTG Leu	CAA Gln	CAC His	ATT Ile	GTG Val	559						
																120			125		130	
GGG Gly	CCA Pro	CAG Gln	CGC Arg	TTC Phe	TCA Ser	GGA Gly	GCT Ala	CCA Pro	GCT Ala	ATG Met	ATG Met	GAA Glu	GGC Gly	TCA Ser	TGG Trp	607						
																135			140		145	
TTG Leu	GAT Asp	GTG Val	GCC Ala	CAG Gln	CGA Arg	GGC Gly	AAG Lys	CCT Pro	GAG Glu	GCC Ala	CAG Gln	CCA Pro	TTT Phe	GCA Ala	CAC His	655						
																155			160		165	
CTC Leu	ACC Thr	ATC Ile	AAT Asn	GCT Ala	GCC Ala	AGC Ser	ATC Ile	CCA Pro	TCG Ser	GGT Gly	TCC Ser	CAT His	AAA Lys	GTC Val	ACT Thr	703						
																170			175		180	
CTG Leu	TCC Ser	TCT Ser	TGG Trp	TAC Tyr	CAC His	GAT Asp	CGA Arg	GGC Gly	TGG Trp	GCC Ala	AAG Lys	ATC Ile	TCT Ser	AAC Asn	ATG Met	751						
																185			190		195	
ACG Thr	TTA Leu	AGC Ser	AAC Asn	GGA Gly	AAA Lys	CTA Leu	AGG Arg	GTT Val	AAC Asn	CAA Gln	GAT Asp	GGC Gly	TTC Phe	TAT Tyr	TAC Tyr	799						
																200			205		210	
CTG Leu	TAC Tyr	GCC Ala	AAC Asn	ATT Ile	TGC Cys	TTT Phe	CGG Arg	CAT His	CAT His	GAA Glu	ACA Thr	TCG Ser	GGA Gly	AGC Ser	GTA Val	847						
																215			220		225	
CCT Pro	ACA Thr	GAC Asp	TAT Tyr	CTT Leu	CAG Gln	CTG Leu	ATG Met	GTG Val	TAT Tyr	GTC Val	GTT Val	AAA Lys	ACC Thr	AGC Ser	ATC Ile	895						
																235			240		245	

AAA ATC CCA AGT TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn 250 255 260	943
TGG TCG GGC AAT TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly 265 270 275	991
TTT TTC AAG CTC CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn 280 285 290	1039
CCT TCC CTG CTG GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe 295 300 305 310	1087
AAA GTT CAG GAC ATA GAC TGAGACTCAT TTCGTGGAAC ATTAGCATGG Lys Val Gln Asp Ile Asp 315	1135
ATGTCCTAGA TGT'TTGAAA CTTCTTAAAA AATGGATGAT GTCTATACAT GTGTAAGACT	1195
ACTAAGAGAC ATGGCCCACG GTGTATGAAA CTCACAGCCC TCTCTCTTGA GCCTGTACAG	1255
GTGTGTGATA TGTAAGTCC ATAGGTGATG TTAGATTATG GGTGATTACA CAACGGTTTT	1315
ACAATTTTGT AATGATTTCC TAGAATTGAA CCAGATTGGG AGAGGTATTC CGATGCTTAT	1375
GAAAACTTA CACGTGAGCT ATGGAAGGGG GTCACAGTCT CTGGGTCTAA CCCCTGGACA	1435
TGTGCCACTG AGAACCTTGA AATTAAGAGG ATGCCATGTC ATTGCAAAGA AATGATAGTG	1495
TGAAGGGTTA AGTTCTTTTG AATTGTTACA TTGCGCTGGG ACCTGCAAAT AAGTTCTTTT	1555
TTTCTAATGA GGAGAGAAAA ATATATGTAT TTTTATATAA TGTCTAAAGT TATATTTTACAG	1615
GTGTAATGTT TTCTGTGCAA AGTTTTGTAA ATTATATTTG TGCTATAGTA TTTGATTCAA	1675
AATATTTTAAA AATGTCTCAC TGTTGACATA TTTAATGTTT TAAATGTACA GATGTATTTA	1735
ACTGGTGCAC TTTGTAATTC CCCTGAAGGT ACTCGTAGCT AAGGGGGCAG AATACTGTTT	1795
CTGGTGACCA CATGTAGTTT ATTTCTTTAT TCTTTTAAAC TTAATAGAGT CTTCAGACTT	1855
GTCAAACTA TGCAAGCAAA ATAAATAAAT AAAAATAAAA TGAATACCTT GAATAATAAG	1915
TAGGATGTTG GTCACCAGGT GCCTTTCAAA TTTAGAAGCT AATTGACTTT AGGAGCTGAC	1975
ATAGCCAAAA AGGATACATA ATAGGCTACT GAAATCTGTC AGGAGTATTT ATGCAATTAT	2035
TGAACAGGTG TCTTTTTTTT CAAGAGCTAC AAATTGTAAA TTTTGTTTCT TTTTTTTCCC	2095
ATAGAAAATG TACTATAGTT TATCAGCCAA AAAACAATCC ACTTTTAAAT TTAGTGAAAG	2155
TTATTTTATT ATACTGTACA ATAAAAGCAT TGTCTCTGAA TGTTAATTTT TTGGTACAAA	2215
AAATAAATTT GTACGAAAAC CTGAAAAAAA AAAAAAAAAA AAAAAAAGG GCGGCCGCTC	2275
TAGAGGGCCC TATTCTATAG	2295

B
cont.

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu
 1 5 10 15
 Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
 20 25 30
 Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Ala Ala Ser Arg Ser
 35 40 45
 Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
 50 55 60
 Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
 65 70 75 80
 Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
 85 90 95
 Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
 100 105 110
 Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
 115 120 125
 Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
 130 135 140
 Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
 145 150 155 160
 Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
 165 170 175
 Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
 180 185 190
 Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
 195 200 205
 Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
 210 215 220
 Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
 225 230 235 240
 Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
 245 250 255
 Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
 260 265 270
 Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
 275 280 285

B1
 cont

Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
290 295 300

Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
305 310 315

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2272 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 185..1135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AAGCTTGGTA CCGAGCTCGG ATCCACTACT CGACCCACGC GTCCGCGCGC CCCAGGAGCC 60
 AAAGCCGGGC TCCAAGTCGG CGCCCCACGT CGAGGCTCCG CCGCAGCCTC CGGAGTTGGC 120
 CGCAGACAAG AAGGGGAGGG AGCGGGAGAG GGAGGAGAGC TCCGAAGCGA GAGGGCCGAG 180
 CGCC ATG CGC CGC GCC AGC AGA GAC TAC ACC AAG TAC CTG CGT GGC TCG 229
 Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser
 1 5 10 15
 GAG GAG ATG GGC GGC GGC CCC GGA GCC CCG CAC GAG GGC CCC CTG CAC 277
 Glu Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His
 20 25 30
 GCC CCG CCG CCG CCT GCG CCG CAC CAG CCC CCC GCC GCC TCC CGC TCC 325
 Ala Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser
 35 40 45
 ATG TTC GTG GCC CTC CTG GGG CTG GGG CTG GGC CAG GTT GTC TGC AGC 373
 Met Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
 50 55 60
 GTC GCC CTG TTC TTC TAT TTC AGA GCG CAG ATG GAT CCT AAT AGA ATA 421
 Val Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
 65 70 75
 TCA GAA GAT GGC ACT CAC TGC ATT TAT AGA ATT TTG AGA CTC CAT GAA 469
 Ser Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu
 80 85 90 95
 AAT GCA GAT TTT CAA GAC ACA ACT CTG GAG AGT CAA GAT ACA AAA TTA 517
 Asn Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu
 100 105 110
 ATA CCT GAT TCA TGT AGG AGA ATT AAA CAG GCC TTT CAA GGA GCT GTG 565
 Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val
 115 120 125

B1
Cont.

CAA AAG GAA TTA CAA CAT ATC GTT GGA TCA CAG CAC ATC AGA GCA GAG Gln Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu 130 135 140	613
AAA GCG ATG GTG GAT GGC TCA TGG TTA GAT CTG GCC AAG AGG AGC AAG Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys 145 150 155	661
CTT GAA GCT CAG CCT TTT GCT CAT CTC ACT ATT AAT GCC ACC GAC ATC Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile 160 165 170 175	709
CCA TCT GGT TCC CAT AAA GTG AGT CTG TCC TCT TGG TAC CAT GAT CGG Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg 180 185 190	757
GGT TGG GCC AAG ATC TCC AAC ATG ACT TTT AGC AAT GGA AAA CTA ATA Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile 195 200 205	805
GTT AAT CAG GAT GGC TTT TAT TAC CTG TAT GCC AAC ATT TGC TTT CGA Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg 210 215 220	853
CAT CAT GAA ACT TCA GGA GAC CTA GCT ACA GAG TAT CTT CAA CTA ATG His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met 225 230 235	901
GTG TAC GTC ACT AAA ACC AGC ATC AAA ATC CCA AGT TCT CAT ACC CTG Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu 240 245 250 255	949
ATG AAA GGA GGA AGC ACC AAG TAT TGG TCA GGG AAT TCT GAA TTC CAT Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His 260 265 270	997
TTT TAT TCC ATA AAC GTT GGT GGA TTT TTT AAG TTA CGG TCT GGA GAG Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu 275 280 285	1045
GAA ATC AGC ATC GAG GTC TCC AAC CCC TCC TTA CTG GAT CCG GAT CAG Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln 290 295 300	1093
GAT GCA ACA TAC TTT GGG GCT TTT AAA GTT CGA GAT ATA GAT Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp 305 310 315	1135
TGAGCCCCAG TTTTGGAGT GTTATGTATT TCCTGGATGT TTGGAAACAT TTTTAAAC	1195
AAGCCAAGAA AGATGTATAT AGGTGTGTGA GACTACTAAG AGGCATGGCC CCAACGGTAC	1255
ACGACTCAGT ATCCATGCTC TTGACCTTGT AGAGAACACG CGTATTTACA GCCAGTGGGA	1315
GATGTTAGAC TCATGGTGTG TTACACAATG GTTTTTTAAAT TTTGTAATGA ATTCCTAGAA	1375
TTAAACCAGA TTGGAGCAAT TACGGGTTGA CCTTATGAGA AACTGCATGT GGGCTATGGG	1435
AGGGGTTGGT CCCTGGTCAT GTGCCCCTTC GCAGCTGAAG TGGAGAGGGT GTCATCTAGC	1495
GCAATTGAAG GATCATCTGA AGGGGCAAAT TCTTTTGAAT TGTTACATCA TGCTGGAACC	1555
TGCAAAAAAT ACTTTTTCTA ATGAGGAGAG AAAATATATG TATTTTTATA TAATATCTAA	1615

81
cont.


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AGTTATATTT CAGATGTAAT GTTTTCTTTG CAAAGTATTG TAAATTATAT TTGTGCTATA 1675
GTATTTGATT CAAAATATTT AAAAATGTCT TGCTGTTGAC ATATTTAATG TTTTAAATGT 1735
ACAGACATAT TTAAC TGGTG CACTTTGTAA ATTCCCTGGG GAAAACTTGC AGCTAAGGAG 1795
GGGAAAAAAA TGTGTGTTTCC TAATATCAAA TGCAGTATAT TTCTTCGTTT TTTTAAAGTT 1855
AATAGATTTT TTCAGACTTG TCAAGCCTGT GCAAAAAAAT TAAATGGAT GCCTTGAATA 1915
ATAAGCAGGA TGTGCGCCAC CAGGTGCCTT TCAAATTTAG AAATAATTG ACTTTAGAAA 1975
GCTGACATTG CAAAAAGGA TACATAATGG GCCACTGAAA TCTGTCAAGA GTAGTTATAT 2035
AATTGTTGAA CAGGTGTTTT TCCACAAGTG CCGCAAATTG TACCTTTTTT TTTTTTTCAA 2095
AATAGAAAAG TTATTAGTGG TTTATCAGCA AAAAAGTCCA ATTTTAATTT AGTAAATGTT 2155
ATCTTATACT GTACAATAAA AACATTGCCT TTGAATGTTA ATTTTGTGGT AAAAAATAA 2215
ATTTATATGA AAAAAAAA AAAAGGGCGG CCGCTCTAGA GGGCCCTATT CTATAGG 2272

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(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu
1 5 10 15
Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala
20 25 30
Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met
35 40 45
Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val
50 55 60
Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser
65 70 75 80
Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
85 90 95
Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
100 105 110
Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
115 120 125
Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
130 135 140
Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
145 150 155 160

Bl
cont.

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
 165 170 175
 Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
 180 185 190
 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
 195 200 205
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
 210 215 220
 His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
 225 230 235 240
 Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
 245 250 255
 Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
 260 265 270
 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu
 275 280 285
 Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
 290 295 300
 Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
 305 310 315

B¹
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